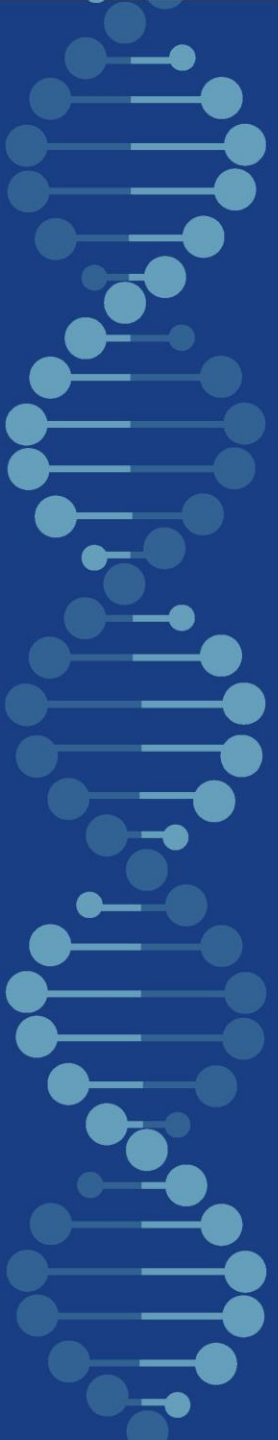


Genomics and Pharmacy and AMS

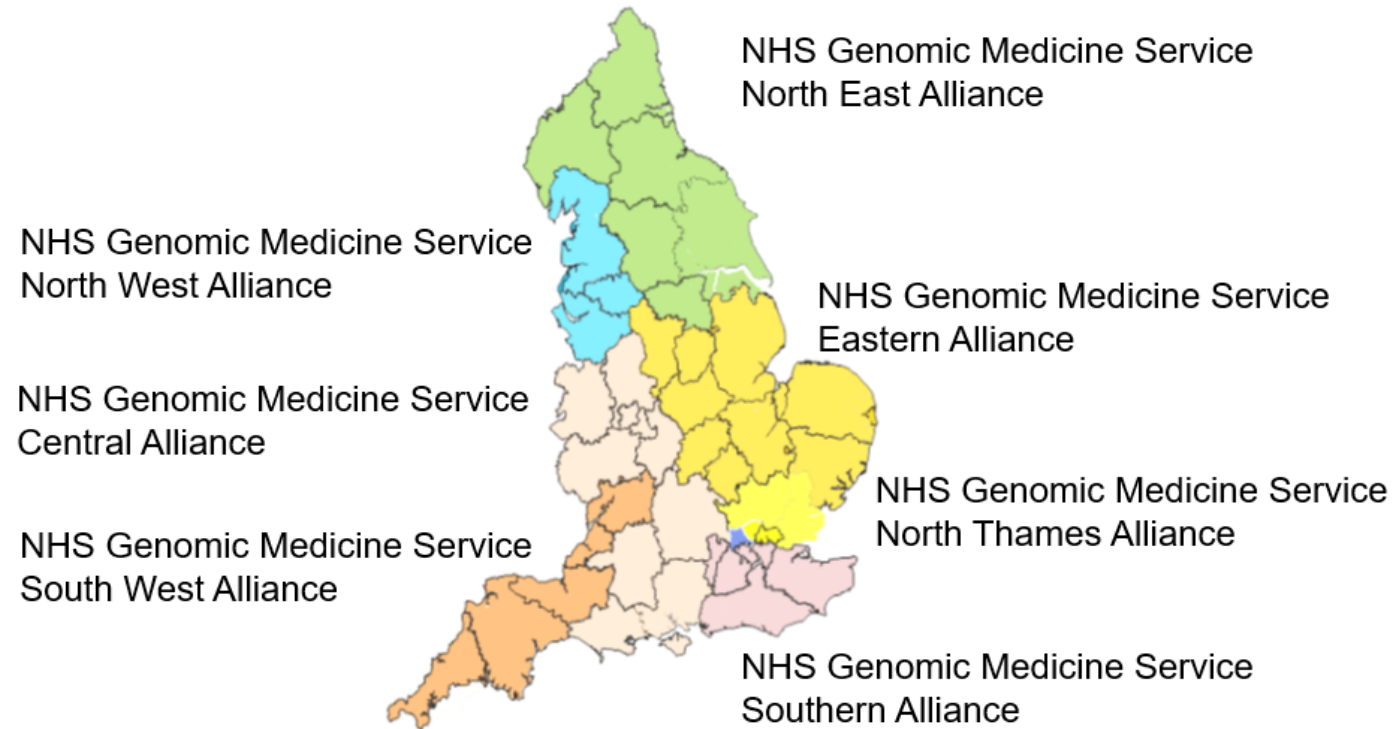
Dr Hayley Wickens

Consultant Pharmacist Genomic Medicine



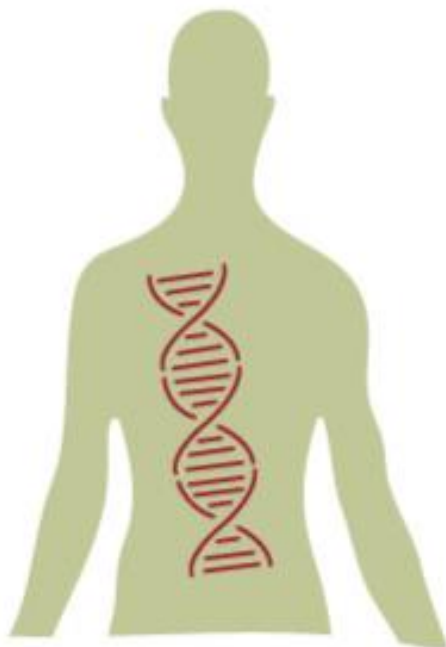
NHS Genomic Medicine Service

- **Regional infrastructures (NHS GMS Alliances)** to support the systematic embedding of genomic medicine
 - National co-ordination and oversight: Genomics Unit in NHSE/I
 - **Specialist pharmacist** and **chief pharmacist** in each GMSA



To personalise treatment and surveillance we can use genomic information...

from a person



- To sub-classify their disease
- To assess their susceptibility
- To predict their response to drugs
- To choose the best treatment

from a person's
cancer



- To make a prognosis
- To target therapy to its genomic profile

from an infective
organism



- To diagnose the type of infection
- To choose appropriate treatment
- To track epidemics

Drug treatment stratification using genomics



Clinical diagnosis
HIV/AIDS

Drug (Abacavir) is known to be beneficial



Approximately 20% of all new prescriptions in UK primary care have an actionable drug-gene interaction (Youssef et al 2021)

<https://bpspubs.onlinelibrary.wiley.com/doi/pdf/10.1111/bcp.14704>



Abacavir
(not toxic)
(3)

Abacavir
(is toxic)
(1)



Example of genomics in AMR testing: TB



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Press release

England world leaders in the use of whole genome sequencing to diagnose TB

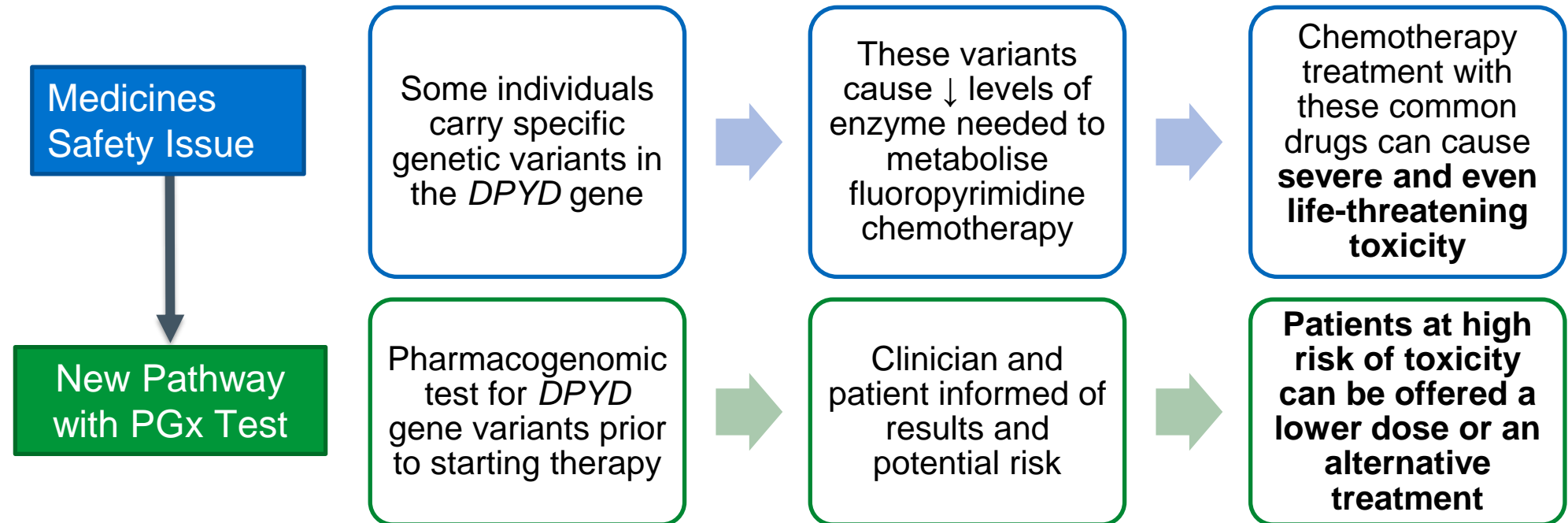
Whole genome sequencing (WGS) is now being used to identify different strains of tuberculosis (TB), announced Public Health England today.

Published 28 March 2017
From: [Public Health England](#)

- “...This is the first time that WGS has been used as a diagnostic solution for managing a disease on this scale anywhere in the world...”
- “... Where previously it could take **up to a month** to confirm a diagnosis of TB, confirm the treatment choices and to detect spread between cases, this can now be done in **just over a week** by PHE’s Birmingham laboratory...”

Example of pharmacogenomic testing: *DPYD*

- *DPYD* pharmacogenomic test offered to all patients prior to starting fluoropyrimidine chemotherapy (5-fluorouracil, capecitabine) – 38k pts/yr



- Anticipated to ↓ severe toxicity (\geq grade 3), ↓ hospitalisation, ↓ deaths, ↓ use of rescue drug

Home > [Drug Safety Update](#)

Flucytosine (Ancotil): new contraindication in patients with DPD deficiency

Flucytosine is a prodrug of 5-fluorouracil used to treat systemic yeast and fungal infections and can cause life-threatening and severe toxicity in patients with complete and partial dihydropyrimidine dehydrogenase (DPD) deficiency. Although pre-testing of DPD status before flucytosine treatment is not required, a new contraindication for patients with complete DPD deficiency has been introduced.

From: [Medicines and Healthcare products Regulatory Agency](#)

Published 22 October 2020

<https://www.gov.uk/drug-safety-update/flucytosine-ancotil-new-contraindication-in-patients-with-dpd-deficiency>



Neonatal gentamicin hearing loss risk – PALOH group (Manchester)

March 21, 2022

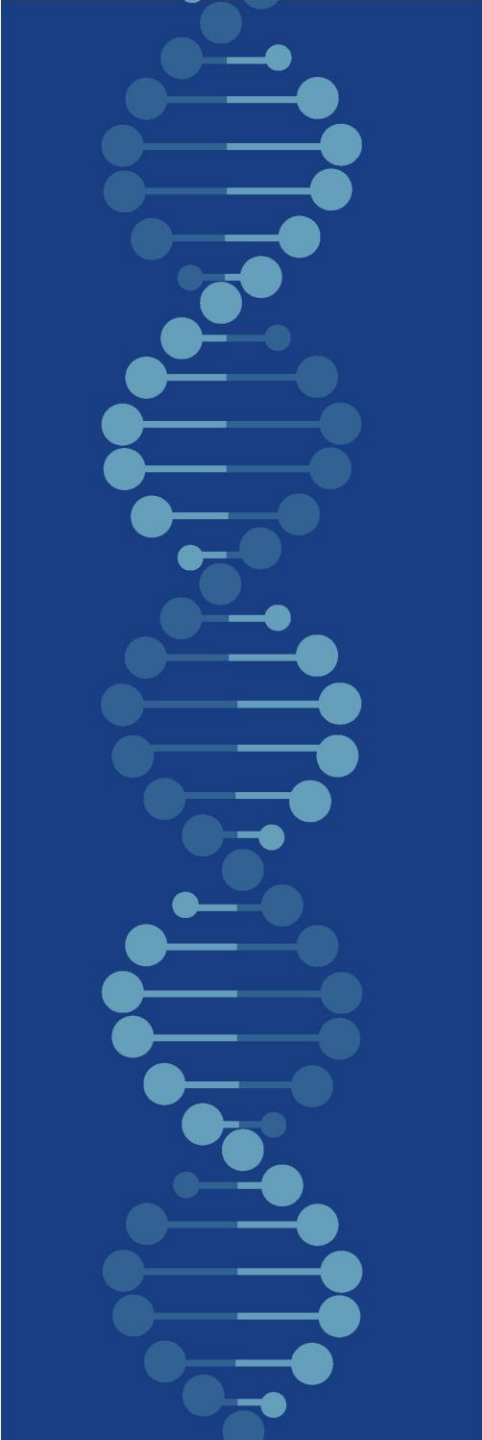
Rapid Point-of-Care Genotyping to Avoid Aminoglycoside-Induced Ototoxicity in Neonatal Intensive Care

John H. McDermott, MD, MRes^{1,2}; Ajit Mahaveer, MD³; Rachel A. James, PhD¹; [et al](#)

» [Author Affiliations](#) | [Article Information](#)

JAMA Pediatr. Published online March 21, 2022. doi:10.1001/jamapediatrics.2022.0187

mtDNA mutation m.1555A>G and risk of hearing loss with aminoglycosides



GOV.UK Top

[Home](#) > [Drug Safety Update](#)

Aminoglycosides (gentamicin, amikacin, tobramycin, and neomycin): increased risk of deafness in patients with mitochondrial mutations

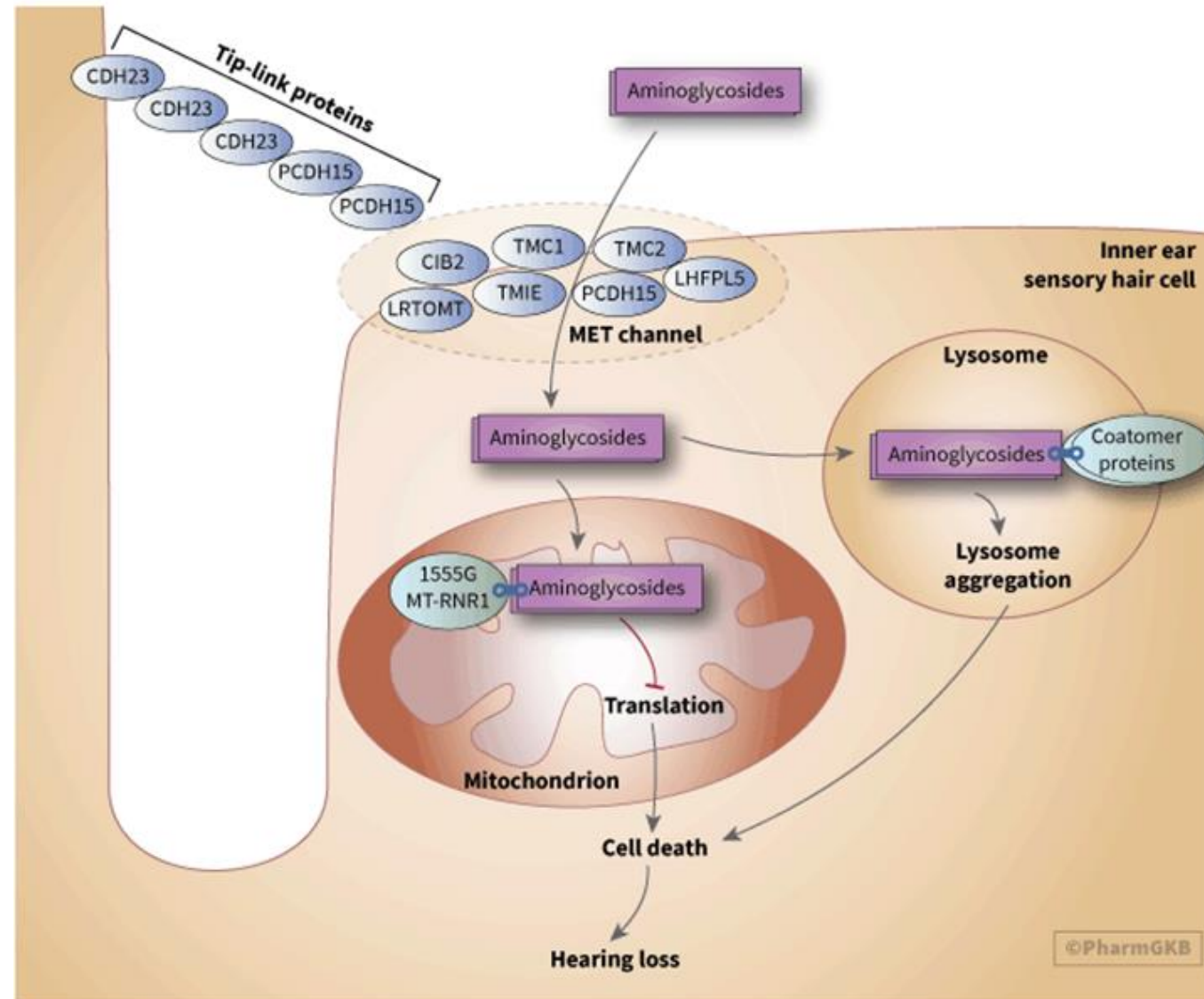
Evidence suggests an increased risk of aminoglycoside-associated ototoxicity in patients with mitochondrial mutations, including cases in which the patient's aminoglycoside serum levels were within the recommended range. These mitochondrial mutations are rare and penetrance is uncertain. Genetic testing should not delay urgently needed aminoglycoside treatment but may be considered, especially before the start of recurrent or long-term treatment.

From: [Medicines and Healthcare products Regulatory Agency](#)
Published 7 January 2021

- Epidemiological studies showing ↑ risk of deafness in patients with m.1555A>G mutation given AG
- Prevalence approx. 1 in 500
- Some w Hx of maternal deafness
- No cases with topical AG (but potentially as same mech)

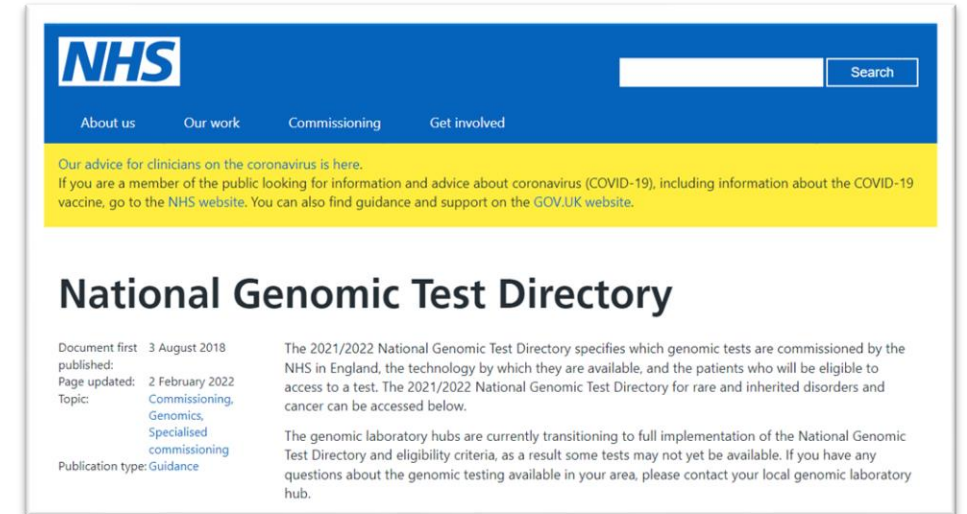
Proposed mechanism of AG ototoxicity

- MT-RNR1 encodes 12S mitochondrial ribosomal subunit
- 12S is a homolog of prokaryotic 16S subunit (AG target)
- Certain variants in MT-RNR1 gene (e.g m.A1555G) make the 12S 'look like' the bacterial 16S
 - AG binds 12S
 - protein synthesis disrupted
 - Cell death
- There are other variants that do this but rarer
 - May see expansion of the variants included in commissioned test



Genomic test approval & commissioning

- NHSEI National Genomic Test Directory
 - Application process, test evaluation working groups
 - Ca/Rare Dis/?PGx



- **PGx: currently only DPYD, aminoglycoside (not POC)**
- Plus genomic tests historically commissioned by other routes e.g. abacavir, carbamazepine

Part IX. Audiology

R65 Aminoglycoside exposure posing risk to hearing

Testing Criteria

Significant exposure to aminoglycosides posing risk of ototoxicity

This indication would be relevant to:

1. individuals with a predisposition to gram negative infections for example due to known respiratory

Significant exposure to aminoglycosides posing risk of ototoxicity

This indication would be relevant to:

1. individuals with a predisposition to gram negative infections for example due to known respiratory disease (e.g. bronchiectasis, cystic fibrosis) or due to structural or voiding genitourinary tract disorders,
OR
2. individuals with hearing loss who have been exposed to aminoglycosides

- Other

Specialist Service Group

- Core

Associated Tests

Code	Name	Optimal Family Structure	Scope(s)	Target Type	Target Name	Method
R65.1	MT-RNR1 1555A>G Targeted mutation testing	Singleton	Small variants	Single interval	MT-RNR1 1555A>G	Targeted mutation testing



A vertical graphic on the left side of the slide, showing a DNA double helix structure. It is composed of blue circles of varying sizes connected by horizontal lines, set against a dark blue background.

Where can I learn more?

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WHAT IS PHARMACOGENOMICS?

The study of the relationship between genetic variations and how our body responds to medications.

[Pretty cool right? Tell me more...](#)

PHARMACOGENOMICS. KNOWLEDGE. IMPLEMENTATION.

PharmGKB is a comprehensive resource that curates knowledge about the impact of genetic variation on drug response for clinicians and researchers.

[Learn more about PharmGKB](#)



<https://cpicpgx.org/genes-drugs/>

(N=448)

- 1 Most recent guideline publication:
[Clinical Pharmacogenetics Implementation Guidelines for Abacavir \(April 2012\)](#)
- 2 Updates since publication:
[May 2014](#): Guideline authors reviewed additional recommendations in the 2012 guideline; therefore evidence table were updated (see below).
- 3 Tables and figure provided in the main manuscript:
Table 1. Assignment of likely HLA-B phenotypes based on HLA-B*57:01 genotype.
Table 2. Recommended therapeutic use of abacavir in relation to HLA-B*57:01 genotype.
Figure 1. Treatment algorithm for clinical use of abacavir based on HLA-B*57:01 genotype.
- 4 Supplement to: [Clinical Pharmacogenetics Implementation Guidelines for Abacavir Dosing \(May 2014\)](#)
- 5 Tables and figures included in the supplementary materials:
Supplemental Table S1. Frequencies of alleles in major HLA-B*57:01 genotypes.
Supplemental Table S2. Detailed table with all reference HLA-B*57:01 genotypes.
Supplemental Table S3. Evidence linking genotypic variability to phenotypic variability indicates a high quality of evidence in the majority of cases (see [Supplementary Table S3](#)).
- 6
- 7
- 8

CPIC® Guideline for

Most recent guideline publication:

[Clinical Pharmacogenetics Implementation Guidelines for Abacavir \(April 2012\)](#)

Updates since publication:

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- Figure 1. Treatment algorithm for clinical use of abacavir based on HLA-B*57:01 genotype.

Supplement to: [Clinical Pharmacogenetics Implementation Guidelines for Abacavir Dosing \(May 2014\)](#)

Tables and figures included in the supplementary materials:

- Supplemental Table S1. Frequencies of alleles in major HLA-B*57:01 genotypes.
- Supplemental Table S2. Detailed table with all reference HLA-B*57:01 genotypes.
- Supplemental Table S3. Evidence linking genotypic variability to phenotypic variability indicates a high quality of evidence in the majority of cases (see [Supplementary Table S3](#)).

Linking genetic variability to variability in drug-related phenotypes

There is substantial evidence linking the presence of the *HLA-B*57:01* genotype with phenotypic variability (see [Supplementary Table S3](#) online). The application of a grading system to the evidence linking genotypic variability to phenotypic variability indicates a high quality of evidence in the majority of cases (see [Supplementary Table S3](#)). The evidence described below and in [Supplementary Table S3](#) provides the basis for the recommendations in [Figure 1](#) and [Table 2](#).

In 2002, two independent research groups reported the initial association between *HLA-B*57:01* and abacavir HSR^{24,25} using cohort and case-control designs. The association was replicated

moreover, the results of PREDICT-1, the first genetic-based, prospective, randomized trial of a genetic test to reduce adverse drug events, showed that genetic prescreening for *HLA-B*57:01* resulted in no immunologically confirmed HSR events among *HLA-B*57:01*-negative patients in the genetic testing arm,³¹ vs. a 2.7% incidence of immunologically confirmed HSR among 842 unscreened patients in the standard-of-care control arm. The results of PREDICT-1 and the existing body of evidence prompted the FDA to implement a black box warning in 2008 about the high risk of *HLA-B*57:01*-associated HSR. The FDA recommended that all patients be screened before being treated with abacavir (including those who had previously tolerated the drug and were being restarted on the therapy) and that abacavir not be initiated in carriers of *HLA-B*57:01*. Abacavir is one of a limited number of drugs for which the FDA has recommended genetic testing prior to use, and it remains one of the best examples to date of pharmacogenetics being integrated into routine medical practice.

Therapeutic recommendations

We agree with others³²⁻³⁶ that *HLA-B*57:01* screening should be performed in all abacavir-naive individuals before initiation of abacavir-containing therapy (see [Table 2](#)); this is consistent with the recommendations of the FDA, the US Department of Health and Human Services, and the European Medicines Agency. In abacavir-naive individuals who are *HLA-B*57:01*-positive, abacavir is not recommended and should be considered only under exceptional circumstances when the potential benefit, based on resistance patterns and treatment history, outweighs the risk. *HLA-B*57:01* genotyping is widely available in the developed world and is considered the standard of care prior to initiating abacavir. Where *HLA-B*57:01* genotyping is not

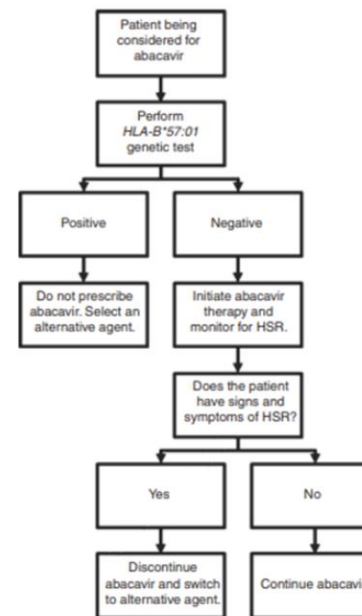


Figure 1 Treatment algorithm for clinical use of abacavir based on *HLA-B*57:01* genotype. HLA-B, human leukocyte antigen B; HSR, abacavir hypersensitivity reaction.

Table 2 Recommended therapeutic use of abacavir in relation to *HLA-B* genotype

Genotype	Implications for phenotypic measures	Recommendations for abacavir	Classification of recommendations ^a
Noncarrier of <i>HLA-B*57:01</i>	Low or reduced risk of abacavir hypersensitivity	Use abacavir per standard dosing guidelines	Strong
Carrier of <i>HLA-B*57:01</i>	Significantly increased risk of abacavir hypersensitivity	Abacavir is not recommended	Strong

HLA-B, human leukocyte antigen B.

^aRating scheme described in [Supplementary Data](#) online.



Review

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Table 1. Genetic association with genes related to antibiotic drug pharmacokinetics.

Gene	Polymorphism	Antibiotic	Effect	Reference
<i>SLC22A8</i>	rs11568482	Cefotaxime (Cephalosporins)	Lower clearance	[33]
<i>ABCC2</i>	rs2273697	Ceftriaxone	Higher drug concentration in CSF	[41]
<i>ABCG2</i>	rs13120400	(Cephalosporins)	Reduction on drug CSF/plasma ratio	
<i>ABCC2</i>	rs717620	Erythromycin	Increase in drug metabolism	[52]
<i>SLCO1B1</i>	rs4149056	(Macrolides)	Reduction in drug metabolism	[53]
<i>ABCB1</i>	2677TT/3435TT	Azithromycin (Macrolides)	Lower C_{max} and higher T_{max}	[55]
<i>UGT1A</i>	rs8175347	Moxifloxacin (Fluoroquinolones)	Lower clearance	[83]
	rs3755319		Higher clearance	
<i>ABCB1</i>	rs2032582		Higher clearance	[83]
<i>ABCB1</i>	rs1045642		Higher T_{max}	[84]
<i>SLCO1B1</i>	rs4149015		Higher AUC_{0-24} and C_{max}	[85]
<i>ABCB1</i>	1236C > T rs1128503 2677G > T/A rs2032582	Daptomycin	Higher AUC_{0-24}	[92]
<i>ABCB1</i>	3435C > T rs1045642 rs1045642	Linezolid	Lower clearance	[97]

Table 2. MHC class I and II polymorphism associations with adverse reaction to antibiotics.

Gene	HLA Association	Antibiotics	Effect	Reference
<i>HLA-DRB1</i>	DRB1*15:01	Amoxicillin clavulanate (Penicillins)	DILI	[16–18]
<i>HLA-DQB1</i>	DQB1*06:14			[19]
<i>HLA-DQB1</i>	rs9274407			[20]
<i>HLA-DRA</i>	rs3135388			[20]
-	rs2523822			[20]
<i>HLA-DRB1-HLA-DQB1</i>	DRB1*15:01-DQB1*06:02			[8,16–18]
<i>HLA-A</i>	A*30:02			[21]
<i>HLA-B</i>	B*18:01			[21]
<i>HLA-B</i>	B*57:01	Flucloxacillin		[24,26]
<i>HLA-B</i>	B*57:03	(Penicillins)		[26]
<i>HLA-A</i>	A*32:01	Vancomycin	DRESS	[88]
<i>HLA-B</i>	B*35:02	Minocycline	DILI	[99]
<i>HLA-B</i>	B*51:01	Clindamycin	Cutaneous reactor	[100]

DILI: drug induced liver injury; DRESS: drug reaction with eosinophilia and systemic sy



Personalised prescribing

Using pharmacogenomics to improve patient outcomes

A report from the Royal College of Physicians and
British Pharmacological Society joint

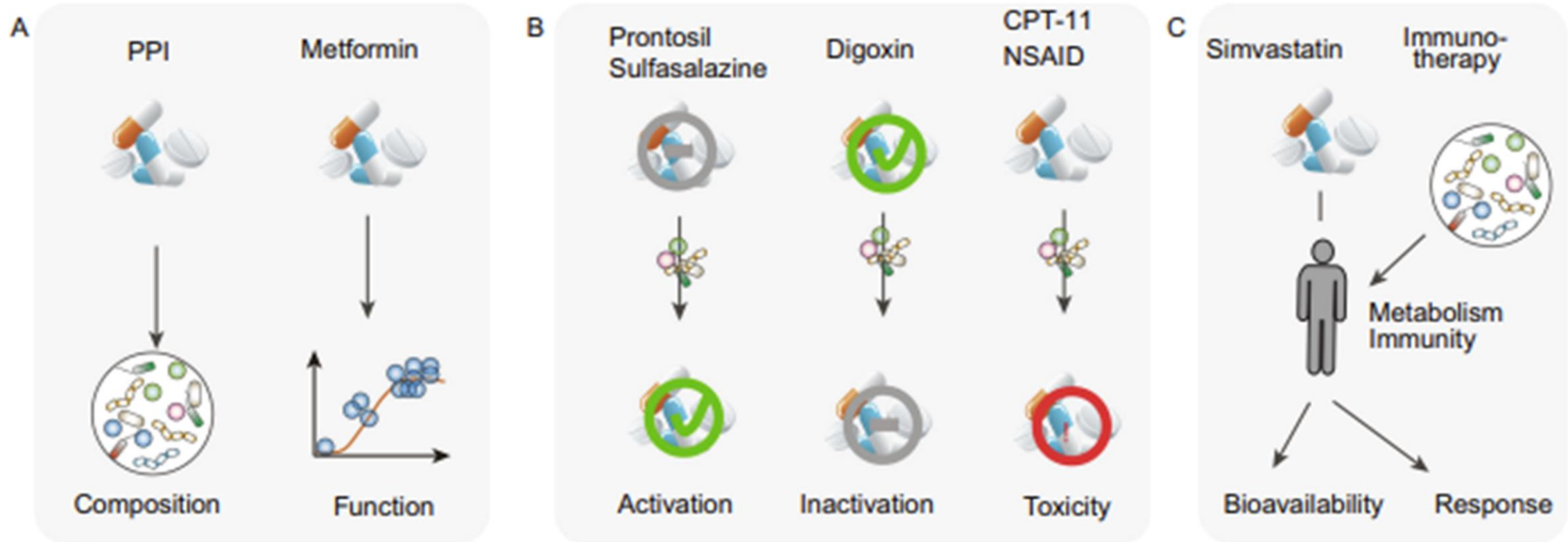
<https://www.rcp.ac.uk/projects/outputs/personalised-prescribing-using-pharmacogenomics-improve-patient-outcomes>

- a pharmacogenomics consult service should be developed within each integrated care system (ICS) led by a multidisciplinary team comprising clinical pharmacologists, pharmacists and other interested specialists, taking into account guidelines and prescribing information. Given that most of the prescribing occurs in primary care, it is important that GPs and pharmacists are considered an essential component of this multidisciplinary pharmacogenomics service



Pharmacomicrobiomics!

Sequencing to model the gut microbiome - Front. Genet., 23
June 2015 | <https://doi.org/10.3389/fgene.2015.00219>



Genomics education for pharmacy teams

- HEE Genomics Education Programme
 - FREE online learning
 - Bite-size courses, modules, full funded MSc available for NHS staff
 - <https://www.genomicseducation.hee.nhs.uk/education/>
- CPPE Genomics module, FutureLearn MOOCs
- GeNotes – new!
- Talk to your GMSA pharmacist or national lead
- National Pharmacy Genomics Workforce Survey
 - All pharmacy staff, all sectors – being analysed



<https://www.genomicseducation.hee.nhs.uk/genotes/>

*launches on 15 June with
In the Clinic Oncology
(and several other
specialties soon to follow)
and more than 60
Knowledge Hub
resources.*





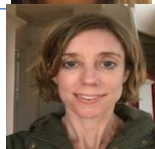

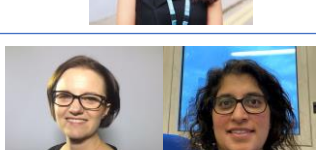


Meet your genomics pharmacist!

(see also Sco, Wal & NI!)



Central and South
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South East	Lucy Galloway Nisha Shaunak 	Lucy.Galloway1@nhs.nhs.uk Nisha.Shaunak@gstt.nhs.uk



A vertical graphic on the left side of the slide depicting a DNA double helix. It is composed of blue circles of varying sizes connected by horizontal lines, set against a dark blue background.

Thank you

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